**PATENT**

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
   THOMAS SPIES AND
   VERONIKA SPIES

Serial No.: Unknown

Filed: May 14, 2001

For: CELL STRESS REGULATED HUMAN
    MHC CLASS 1 GENE

Group Art Unit: 1644

Examiner: DIBRINO. M

Atty. Dkt. No.: FHCC:003USC1

### REQUEST FOR TRANSFER OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821(e)

**BOX SEQUENCE**
Commissioner for Patents
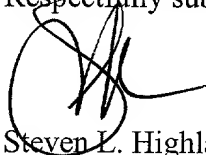Washington, D.C. 20231

Commissioner:

Pursuant to 37 C.F.R. § 1.821(e), Applicants respectfully request that the sequence information previously submitted in parent application ("parent application"), U.S. Serial No. 09/303,161 filed April 29, 1999, be transferred to and used in the above-referenced patent application ("instant application"). Only one computer readable sequence listing was submitted to the U.S. Patent and Trademark Office in the parent application. The sequence information in the instant application is identical to the sequence information contained in the previously-filed computer readable sequence listing in the parent application. It is understood that the U.S. Patent and Trademark Office will make the necessary change in application number and filing date of

25030689.1

the computer readable form that will be used for the instant application. A paper copy of the sequence listing is included in the originally-filed specification of the instant application.

Applicants request the transfer of the previously-filed computer readable sequence listing from the parent application to the instant application is in lieu of filing a duplicate computer readable sequence listing.

No fee is believed to be due in connection with the filing of this document; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be deemed necessary for any reason relating to this document, the Commissioner is hereby authorized to deduct said fee from Fulbright & Jaworski Account No.: 50-1212/10008888/SLH.

Respectfully submitted,

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Austin, Texas 78701
(512) 536-3184

Date: May 14, 2001

# SEQUENCE LISTING

(1)  GENERAL INFORMATION:

    (i)  APPLICANT:
        (A)  NAME: Fred Hutchinson Cancer Research Center, Inc.
        (B)  STREET: 1100 Fairview Avenue North, Mailstop c2M-027
        (C)  CITY: Seattle
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        (E)  COUNTRY: USA
        (F)  POSTAL CODE (ZIP): 98109

        (A)  NAME: Thomas Spies
        (B)  STREET: 2429 E. Aloha
        (C)  CITY: Seattle
        (D)  STATE: Washington
        (E)  COUNTRY: USA
        (F)  POSTAL CODE (ZIP): 98112

        (A)  NAME: Veronika Spies
        (B)  STREET: 2429 E. Aloha
        (C)  CITY: Seattle
        (D)  STATE: Washington
        (E)  COUNTRY: USA
        (F)  POSTAL CODE (ZIP): 98112

    (ii)  TITLE OF INVENTION: CELL STRESS REGULATED HUMAN MHC CLASS I GENE

    (iii)  NUMBER OF SEQUENCES: 16

    (iv)  COMPUTER READABLE FORM:
        (A)  MEDIUM TYPE: Floppy disk
        (B)  COMPUTER: IBM PC compatible
        (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
        (D)  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

    (vi)  PRIOR APPLICATION DATA:
        (A)  APPLICATION NUMBER: US 60/029,044
        (B)  FILING DATE: 29-OCT-1996


(2)  INFORMATION FOR SEQ ID NO: 1:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 11722 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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(2)  INFORMATION FOR SEQ ID NO: 2:

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          (A)  LENGTH: 385 amino acids
          (B)  TYPE: amino acid
          (C)  STRANDEDNESS:
          (D)  TOPOLOGY: linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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```

```
Val His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Cys
    50              55              60
```

```
Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys
65              70              75                      80
```

```
Thr Trp Asp Arg Glu Thr Arg Asp Leu Thr Gly Asn Gly Lys Asp Leu
            85              90                      95
```

```
Arg Met Thr Leu Ala His Ile Lys Asp Gln Lys Glu Gly Leu His Ser
            100             105             110
```

```
Leu Gln Glu Ile Arg Val Cys Glu Ile His Glu Asp Asn Ser Thr Arg
        115             120             125
```

```
Ser Ser Gln His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn
        130             135             140
```

```
Val Glu Thr Glu Glu Trp Thr Val Pro Gln Ser Ser Arg Ala Gln Thr
145             150             155             160
```

```
Leu Ala Met Asn Val Arg Asn Phe Leu Lys Glu Asp Ala Met Lys Thr
            165             170             175
```

```
Lys Thr His Tyr His Ala Met His Ala Asp Cys Leu Gln Glu Leu Arg
            180             185             190
```

```
Arg Tyr Leu Glu Ser Ser Val Val Leu Arg Arg Arg Val Pro Pro Met
        195             200             205
```

```
Val Asn Val Thr Arg Ser Glu Ala Ser Glu Gly Asn Ile Thr Val Thr
        210             215             220
```

```
Cys Arg Ala Ser Ser Phe Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg
225             230             235             240
```

```
Gln Asp Gly Val Ser Leu Ser His Asp Thr Gln Gln Trp Gly Asp Val
            245             250             255
```

```
Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile
            260             265             270
```

```
Cys Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly
        275             280             285
```

```
Asn His Ser Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln
        290             295             300
```

```
Ser His Trp Gln Thr Phe His Val Ser Ala Val Ala Ala Ala Ala Ala
305             310             315             320
```

```
Ala Ile Phe Val Ile Ile Ile Phe Tyr Val Arg Cys Cys Lys Lys Lys
            325             330             335
```

```
Thr Ser Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp
            340             345             350
```

```
Gln His Pro Val Gly Thr Ser Asp His Arg Asp Ala Thr Gln Leu Gly
        355                 360                 365

Phe Gln Pro Leu Met Ser Ala Leu Gly Ser Thr Gly Ser Thr Glu Gly
        370                 375                 380

Ala
385
```

(2)  INFORMATION FOR SEQ ID NO: 3:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 2380 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
GGGCCATGGG GCTGGGCCGG GTCCTGCTGT TTCTGGCCGT CGCCTTCCCT TTTGCACCCC      60

CGGCAGCCGC CGCTGAGCCC CACAGTCTTC GTTACAACCT CATGGTGCTG TCCCAGGATG     120

AATCTGTGCA GTCAGGGTTT CTCGCTGAGG GACATCTGGA TGGTCAGCCC TTCCTGCGCT     180

ATGACAGGCA GAAACGCAGG GCAAAGCCCC AGGGACAGTG GGCAGAAGAT GTCCTGGGAG     240

CTAAGACCTG GGACACAGAG ACCGAGGACT TGACAGAGAA TGGGCAAGAC CTCAGGAGGA     300

CCCTGACTCA TATCAAGGAC CAGAAAGGAG GCTTGCATTC CCTCCAGGAG ATTAGGGTCT     360

GTGAGATCCA TGAAGACAGC AGCACCAGGG GCTCCCGGCA TTTCTACTAC GATGGGGAGC     420

TCTTCCTCTC CCAAAACCTG GAGACTCAAG AATCGACAGT GCCCCAGTCC TCCAGAGCTC     480

AGACCTTGGC TATGAACGTC ACAAATTTCT GGAAGGAAGA TGCCATGAAG ACCAAGACAC     540

ACTATCGCGC TATGCAGGCA GACTGCCTGC AGAAACTACA GCGATATCTG AAATCCGGGG     600

TGGCCATCAG GAGAACAGTG CCCCCCATGG TGAATGTCAC CTGCAGCGAG GTCTCAGAGG     660

GCAACATCAC CGTGACATGC AGGGCTTCCA GCTTCTATCC CCGGAATATC ACACTGACCT     720

GGCGTCAGGA TGGGGTATCT TTGAGCCACA ACACCCAGCA GTGGGGGGAT GTCCTGCCTG     780

ATGGGAATGG AACCTACCAG ACCTGGGTGG CCACCAGGAT TCGCCAAGGA GAGGAGCAGA     840

GGTTCACCTG CTACATGGAA CACAGCGGGA TCACGGCAC TCACCCTGTG CCCTCTGGGA     900

AGGTGCTGGT GCTTCAGAGT CAACGGACAG ACTTTCCATA TGTTTCTGCT GCTATGCCAT     960

GTTTTGTTAT TATTATTATT CTCTGTGTCC CTTGTTGCAA GAAGAAAACA TCAGCGGCAG    1020

AGGGTCCAGA GCTTGTGAGC CTGCAGGTCC TGGATCAACA CCCAGTTGGG ACAGGAGACC    1080

ACAGGGATGC AGCACAGCTG GGATTTCAGC CTCTGATGTC AGCTACTGGG TCCACTGGTT    1140
```

```
CCACTGAGGG CGCCTAGACT CTACAGCCAG GCGGCCAGGA TTCAACTCCC TGCCTGGATC    1200

TCACCAGCAC TTTCCCTCTG TTTCCTGACC TATGAAACAG AAAATAACAT CACTTATTTA    1260

TTGTTGTTGG ATGCTGCAAA GTGTTAGTAG GTATGAGGTG TTTGCTGCTC TGCCACGTAG    1320

AGAGCCAGCA AAGGGATCAT GACCAACTCA ACATTCCATT GGAGGCTATA TGATCAAACA    1380

GCAAATTGTT TATCATGAAT GCAGGATGTG GGCAAACTCA CGACTGCTCC TGCCAACAGA    1440

AGGTTTGCTG AGGGCATTCA CTCCATGGTG CTCATTGGAG TTATCTACTG GGTCATCTAG    1500

AGCCTATTGT TTGAGGAATG CAGTCTTACA AGCCTACTCT GGACCCAGCA GCTGACTCCT    1560

TCTTCCACCC CTCTTCTTGC TATCTCCTAT ACCAATAAAT ACGAAGGGCT GTGGAAGATC    1620

AGAGCCCTTG TTCACGAGAA GCAAGAAGCC CCCTGACCCC TTGTTCCAAA TATACTCTTT    1680

TGTCTTTCTC TTTATTCCCA CGTTCGCCCT TTGTTCAGTC CAATACAGGG TTGTGGGGCC    1740

CTTAACAGTG CCATATTAAT TGGTATCATT ATTTCTGTTG TTTTTGTTTT TGTTTTTGTT    1800

TTTGTTTTTG AGACAGAGTC TCACTCGTCA CCCAGGCTGC AGTTCACTGG TGTGATCTCA    1860

GCTCACTGCA ACCTCTGCCT CCCAGGTTCA AGCACTTCTC GTACCTCAGA CTCCCGATAG    1920

CTGGGATTAC AGACAGGCAC CACCACACCC AGCTAATTTT TGTATTTTTT GTAGAGACGG    1980

GGTTTCGCCA AGTTGACCAG CCCAGTTTCA AACTCCTGAC CTCAGGTGAT CTGCCTGCCT    2040

TGGCATCCCA AAGTGCTGGG ATTACAAGAA TGAGCCACCG TGCCTGGCCT ATTTTATTAT    2100

ATTGTAATAT ATTTTATTAT ATTAGCCACC ATGCCTGTCC TATTTTCTTA TGTTTTAATA    2160

TATTTTAATA TATTACATGT GCAGTAATTA GATTATCATG GGTGAACTTT ATGAGTGAGT    2220

ATCTTGGTGA TGACTCCTCC TGACCAGCCC AGGACCAGCT TTCTTGTCAC CTTGAGGTCC    2280

CCTCGCCCCG TCACACCGTT ATCGATTACT CTGTGTCTAC TATTATGTGT GCATAATTTA    2340

TACCGTAAAT GTTTACTCTT TAAATAAAAA AAAAAAAAA                          2380
```

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 383 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Gly Leu Gly Arg Val Leu Leu Phe Leu Ala Val Ala Phe Pro Phe
1               5                   10                  15

Ala Pro Pro Ala Ala Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu
            20                  25                  30
```

Met Val Leu Ser Gln Asp Glu Ser Val Gln Ser Gly Phe Leu Ala Glu
       35                40               45

Gly His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg
    50               55              60

Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Ala Lys
65               70             75              80

Thr Trp Asp Thr Glu Thr Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu
          85            90             95

Arg Arg Thr Leu Thr His Ile Lys Asp Gln Lys Gly Gly Leu His Ser
        100           105           110

Leu Gln Glu Ile Arg Val Cys Glu Ile His Glu Asp Ser Ser Thr Arg
       115          120          125

Gly Ser Arg His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn
    130           135           140

Leu Glu Thr Gln Glu Ser Thr Val Pro Gln Ser Ser Arg Ala Gln Thr
145               150          155          160

Leu Ala Met Asn Val Thr Asn Phe Trp Lys Glu Asp Ala Met Lys Thr
        165           170          175

Lys Thr His Tyr Arg Ala Met Gln Ala Asp Cys Leu Gln Lys Leu Gln
        180           185          190

Arg Tyr Leu Lys Ser Gly Val Ala Ile Arg Arg Thr Val Pro Pro Met
        195          200          205

Val Asn Val Thr Cys Ser Glu Val Ser Glu Gly Asn Ile Thr Val Thr
    210           215           220

Cys Arg Ala Ser Ser Phe Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg
225               230          235          240

Gln Asp Gly Val Ser Leu Ser His Asn Thr Gln Gln Trp Gly Asp Val
        245           250          255

Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile
        260           265          270

Arg Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly
        275           280          285

Asn His Gly Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln
    290           295           300

Ser Gln Arg Thr Asp Phe Pro Tyr Val Ser Ala Ala Met Pro Cys Phe
305               310          315          320

Val Ile Ile Ile Ile Leu Cys Val Pro Cys Cys Lys Lys Lys Thr Ser
        325           330          335

```
Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp Gln His
        340               345               350
```

```
Pro Val Gly Thr Gly Asp His Arg Asp Ala Ala Gln Leu Gly Phe Gln
        355               360               365
```

```
Pro Leu Met Ser Ala Thr Gly Ser Thr Gly Ser Thr Glu Gly Ala
    370               375               380
```

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACTGGGGAAC AAGGTTTATA TGAGA                                          25

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGTCACCCGT CTTCTACAGG ACCC                                           24

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGGCCATGG GGCTGGG                                                   17

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATCTGAGATG TCGGTCC                                                    17


(2) INFORMATION FOR SEQ ID NO: 9:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 25 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGTTCTTGTC CCTTTGCCCG TGTGC                                           25


(2) INFORMATION FOR SEQ ID NO: 10:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 25 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AACCCTTCCC TTACCCCCGT CGTAG                                           25


(2) INFORMATION FOR SEQ ID NO: 11:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 45 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TATGTAAAAC GACGGCCAGT TTCACCTGTG ATTTCCTCTT CCCCA                     45


(2) INFORMATION FOR SEQ ID NO: 12:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 45 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTCTTTTCA ATCCCCGTCT CTCGTCCAGT ATCGACAAAG GACAT                     45


(2) INFORMATION FOR SEQ ID NO: 13:

         (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH: 40 base pairs
               (B)  TYPE: nucleic acid
               (C)  STRANDEDNESS: single
               (D)  TOPOLOGY: linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATGTAAAAC GACGGCCAGT TTCGGGAATG GAGAAGTCAC                              40


(2)  INFORMATION FOR SEQ ID NO: 14:

         (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH: 40 base pairs
               (B)  TYPE: nucleic acid
               (C)  STRANDEDNESS: single
               (D)  TOPOLOGY: linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CGAGAGGAGA GGGAGGTTAA CCAGTATCGA CAAAGGACAT                              40


(2)  INFORMATION FOR SEQ ID NO: 15:

         (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH: 40 base pairs
               (B)  TYPE: nucleic acid
               (C)  STRANDEDNESS: single
               (D)  TOPOLOGY: linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TATGTAAAAC GACGGCCAGT GTTCCTCTCC CCTCCTTAGA                              40


(2)  INFORMATION FOR SEQ ID NO: 16:

         (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH: 41 base pairs
               (B)  TYPE: nucleic acid
               (C)  STRANDEDNESS: single
               (D)  TOPOLOGY: linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AAAAAGTCCC TTTCACGACC ACCAGTATCG ACAAAGGACA T                            41